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Fig. 13-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of "original" pig-baboon chimeric uricase ("PBC") vs. pig uricase

"PBC" uricase:

Pig cDNA from 1 to 674 (Apa site) then Baboon cDNA from 675 to 915 (end). PBC chimeric cDNA can be cut out with NcoI plus BamHI

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 8770 Length: 915
Ratio: 9.585 Gaps: 0
Percent Similarity: 97.814 Percent Identity: 97.814

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

PBC.seq x pig.seq July 25, 1998 08:10 ..

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PBC   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||
PIG   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||

51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||
51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||

101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||
101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||

151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||
151 TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||

201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||
201 TACAGACACCATCAAGAACACAGTTAATGTCCTGGCGAAGTTCAAAGGCA 250
      |||

251 TCAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||
251 TCAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTCCTTTCT 300
      |||

301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||
301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||

351 GAAGCGTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTTATA 400
      |||
351 GAAGCGTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTTATA 400
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Fig. 13-2

401 CTCCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
|||
401 CTCCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
|||
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAACAACCCA 500
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
|||
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAATGGCGCTACCAC 600
|||
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAATGGCGCTACCAC 600
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
|||
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
651 TGTCTCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCACCT 700
|||
651 TGTCTCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
701 CTGTGCAGAAGACCCTCTATGATATCCAGGTGCTCTCCCTGAGCCGAGTT 750
|||
701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAACATTCACTACTTCAA 800
|||
751 CCTGAGATAGAAGATATGGAAATCAGCCTGCCAAATATTCACTACTTAA 800
801 TATAGACATGTCCAAAATGGGTCTGATCAACAAGGAAGAGGTCTTGCTGC 850
|||
801 CATAGACATGTCCAAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
851 CATTAGACAATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
|||
851 CTTTAGACAATCCATATGGCAGGATTACTGGTACAGTCAAGAGGAAGCTG 900
901 TCTTCAAGACTGTGA 915
|||
901 ACTTCAAGGCTGTGA 915

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Fig. 14-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of "original" pig-baboon chimeric uricase ("PBC") vs. baboon uricase

"PBC" uricase:

Pig cDNA from 1 to 674 (Apa site) then Baboon cDNA from 675 to 915 (end). PBC chimeric cDNA can be cut out with NcoI plus BamHI

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 7839 Length: 915
Ratio: 8.567 Gaps: 0
Percent Similarity: 92.459 Percent Identity: 92.459

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

PBC.seq x Wubaboon.seq July 25, 1998 09:36 ..

```

PBC   1 ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT 50
      |||||  |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Bab   1 ATGGCCGACTACCATAACAATAAAAAAGAATGATGAATTGGAGTTTGT 50
      |||||  |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

      51 CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG 100
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
      51 CCGAACTGGCTATGGGAAGGATATGGTAAAAGTTCTCCATATTCAGCGAG 100
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT 150
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     101 ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTTACT 150
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     151 TTGAGCTCCAAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC 200
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     151 CTGAGTTCCAAAAAAGATTACCTGCATGGAGATAATTCAGATATCATCCC 200
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     201 TACAGACACCATCAAGAACACAGTTAATGTCTTGGCGAAGTTCAAAGGCA 250
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     201 TACAGACACCATCAAGAACACAGTTCATGTCTTGGCAAAGTTTAAGGGAA 250
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     251 TCAAAAGCATAGAACTTTTGCTGTGACTATCTGTGAGCATTTTCTTTCT 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     251 TCAAAAGCATAGAAAGCCTTTGGTGTGAATATTTGTGAGTATTTTCTTTCT 300
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     301 TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTG 350
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     301 TCTTTTAACCATGTAATCCGAGCTCAAGTCTACGTGGAAGAAATCCCTTG 350
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

     351 GAAGCGTTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTTATA 400
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
     351 GAAGCGTCTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTTATTCACA 400
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
  
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